STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _10/048,116A_

Source: _1Fw/16_

Date Processed by STIC: _12/29/05_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO **REDUCE** ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.2.2 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
      http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (**<http://www.uspto.gov/ebc/efs/downloads/documents.htm>** , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05): U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: _10/048,116A_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1____Wrapped Nucleics
Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2____Invalid Line Length

The rules require that a line **not exceed** 72 characters in length. This includes white spaces.

3____Misaligned Amino
Numbering

The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.

4____Non-ASCII

The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**

5____Variable Length

Sequence(s)____contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6_✓_PatentIn 2.0
"bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _2,4,6,8_. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

7____Skipped Sequences
(OLD RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for **each** skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.

8____Skipped Sequences
(NEW RULES)

Sequence(s) _____ missing. If **intentional**, please insert the following lines for **each** skipped sequence.
<210> sequence id number
<400> sequence id number
000

9____Use of n's or Xaa's
(NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.

10____Invalid <213>
Response

Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence

11____Use of <220>

Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12____PatentIn 2.0
"bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13____Misuse of n/Xaa

"n" can **only** represent a single nucleotide; "Xaa" can **only** represent a single amino acid

AMC – Biotechnology Systems Branch – 09/09/2003

IFW16

```
RAW SEQUENCE LISTING              DATE: 12/29/2005
PATENT APPLICATION:  US/10/048,116A       TIME: 12:20:15

Input Set : A:\seq list.txt
Output Set: N:\CRF4\12292005\J048116A.raw
```

```
 3 <110> APPLICANT: CNRS
 5 <120> TITLE OF INVENTION: RECOMBINANT PROTEINS AND MOLECULAR COMPLEXES DERIVED
 6       FROM THESE PROTEINS, ANALOGOUS TO MOLECULES INVOLVED IN
 7       IMMUNE RESPONSES
 9 <130> FILE REFERENCE: 1721-47
11 <140> CURRENT APPLICATION NUMBER: 10/048,116A
12 <141> CURRENT FILING DATE: 2002-02-27
14 <150> PRIOR APPLICATION NUMBER: PCT/FR00/02193
15 <151> PRIOR FILING DATE: 2000-07-28
17 <150> PRIOR APPLICATION NUMBER: FR99/09862
18 <151> PRIOR FILING DATE: 1999-07-29
20 <160> NUMBER OF SEQ ID NOS: 8
22 <170> SOFTWARE: PatentIn Ver. 2.0
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 1517
26 <212> TYPE: DNA
27 <213> ORGANISM: Artificial Sequence
29 <220> FEATURE:
30 <223> OTHER INFORMATION: Description of Artificial Sequence: construct
31       coding IAalpha(d)/Fc
33 <220> FEATURE:
34 <221> NAME/KEY: CDS
35 <222> LOCATION: (18)..(1502)
37 <400> SEQUENCE: 1
38 aaagggggga attcagg atg ccg tgc agc aga gct ctg att ctg ggg gtc    50
39                     Met Pro Cys Ser Arg Ala Leu Ile Leu Gly Val
40                      1               5                  10
42 ctc gcc ctg aac acc atg ctc agc ctc tgc gga ggt gaa gac gac att    98
43 Leu Ala Leu Asn Thr Met Leu Ser Leu Cys Gly Gly Glu Asp Asp Ile
44              15                  20                  25
46 gag gcc gac cac gta ggc ttc tat ggt aca act gtt tat cag tct cct   146
47 Glu Ala Asp His Val Gly Phe Tyr Gly Thr Thr Val Tyr Gln Ser Pro
48          30                  35                  40
50 gga gac att ggc cag tac aca cat gaa ttt gat ggt gat gag ttg ttc   194
51 Gly Asp Ile Gly Gln Tyr Thr His Glu Phe Asp Gly Asp Glu Leu Phe
52      45                  50                  55
54 tat gtg gac ttg gat aag aag aaa act gtc tgg agg ctt cct gag ttt   242
55 Tyr Val Asp Leu Asp Lys Lys Lys Thr Val Trp Arg Leu Pro Glu Phe
56  60                  65                  70                  75
58 ggc caa ttg ata ctc ttt gag ccc caa ggt gga ctg caa aac ata gct   290
59 Gly Gln Leu Ile Leu Phe Glu Pro Gln Gly Gly Leu Gln Asn Ile Ala
60                  80                  85                  90
62 gca gaa aaa cac aac ttg gga atc ttg act aag agg tca aat ttc acc   338
```

RAW SEQUENCE LISTING   DATE: 12/29/2005
PATENT APPLICATION: US/10/048,116A   TIME: 12:20:15

Input Set : A:\seq list.txt
Output Set: N:\CRF4\12292005\J048116A.raw

```
63 Ala Glu Lys His Asn Leu Gly Ile Leu Thr Lys Arg Ser Asn Phe Thr
64          95              100          Lys     105
66 cca gct acc aat gag gct cct caa gcg act gtg ttc ccc aag tcc cct   386
67 Pro Ala Thr Asn Glu Ala Pro Gln Ala Thr Val Phe Pro Lys Ser Pro
68          110              115              120
70 gtg ctg ctg ggt cag ccc aac acc ctt atc tgc ttt gtg gac aac atc   434
71 Val Leu Leu Gly Gln Pro Asn Thr Leu Ile Cys Phe Val Asp Asn Ile
72          125              130              135
74 ttc cca cct gtg atc aac atc aca tgg ctc aga aat agc aag tca gtc   482
75 Phe Pro Pro Val Ile Asn Ile Thr Trp Leu Arg Asn Ser Lys Ser Val
76 140              145              150              155
78 aca gac ggc gtt tat gag acc agc ttc ctc gtc aac cgt gac cat tcc   530
79 Thr Asp Gly Val Tyr Glu Thr Ser Phe Leu Val Asn Arg Asp His Ser
80          160              165              170
82 ttc cac aag ctg tct tat ctc acc ttc atc cct tct gat gat gac att   578
83 Phe His Lys Leu Ser Tyr Leu Thr Phe Ile Pro Ser Asp Asp Asp Ile
84          175              180              185
86 tat gac tgc aag gtg gag cac tgg ggc ctg gag gag ccg gtt ctg aaa   626
87 Tyr Asp Cys Lys Val Glu His Trp Gly Leu Glu Glu Pro Val Leu Lys
88          190              195              200
90 cac tgg gaa cct gag att cca gcc ccc atg tca gag ctg aca gaa act   674
91 His Trp Glu Pro Glu Ile Pro Ala Pro Met Ser Glu Leu Thr Glu Thr
92          205              210              215
94 gga ggt gga gga tcc act aca gct cca tca gct cag ctc gaa aaa gag   722
95 Gly Gly Gly Gly Ser Thr Thr Ala Pro Ser Ala Gln Leu Glu Lys Glu
96 220              225              230              235
98 ctc cag gcc ctg gag aag gaa aat gca cag ctg gaa tgg gag ttg caa   770
99 Leu Gln Ala Leu Glu Lys Glu Asn Ala Gln Leu Glu Trp Glu Leu Gln
100             240              245              250
102 gca ctg gaa aag gaa ctg gct cag gca gca tct gag ccc aga ggg ccc  818
103 Ala Leu Glu Lys Glu Leu Ala Gln Ala Ala Ser Glu Pro Arg Gly Pro
104             255              260              265
106 aca atc aag ccc tgt cct cca tgc aaa tgc cca gca cct aac ctc ttg  866
107 Thr Ile Lys Pro Cys Pro Pro Cys Lys Cys Pro Ala Pro Asn Leu Leu
108             270              275              280
110 ggt gga cca tcc gtc ttc atc ttc cct cca aag atc aag gat gta ctc  914
111 Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Ile Lys Asp Val Leu
112         285              290              295
114 atg atc tcc ctg agc ccc ata gtc aca tgt gtg gtg gtg gat gtg agc  962
115 Met Ile Ser Leu Ser Pro Ile Val Thr Cys Val Val Val Asp Val Ser
116 300             305              310              315
118 gag gat gac cca gat gtc cag atc agc tgg ttt gtg aac aac gtg gaa  1010
119 Glu Asp Asp Pro Asp Val Gln Ile Ser Trp Phe Val Asn Asn Val Glu
120             320              325              330
122 gta cac aca gct cag aca caa acc cat aga gag gat tac aac agt act  1058
123 Val His Thr Ala Gln Thr Gln Thr His Arg Glu Asp Tyr Asn Ser Thr
124             335              340              345
126 ctc cgg gtg gtc agt gcc ctc ccc atc cag cac cag gac tgg atg agt  1106
127 Leu Arg Val Val Ser Ala Leu Pro Ile Gln His Gln Asp Trp Met Ser
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RAW SEQUENCE LISTING   DATE: 12/29/2005
PATENT APPLICATION: US/10/048,116A   TIME: 12:20:15

Input Set : A:\seq list.txt
Output Set: N:\CRF4\12292005\J048116A.raw

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128        350               355               360
130 ggc aag gag ttc aaa tgc aag gtc aac aac aaa gac ctc cca gcg ccc    1154
131 Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Asp Leu Pro Ala Pro
132    365               370               375
134 atc gag aga acc atc tca aaa ccc aaa ggg tca gta aga gct cca cag    1202
135 Ile Glu Arg Thr Ile Ser Lys Pro Lys Gly Ser Val Arg Ala Pro Gln
136 380               385               390               395
138 gta tat gtc ttg cct cca cca gaa gaa gag atg act aag aaa cag gtc    1250
139 Val Tyr Val Leu Pro Pro Pro Glu Glu Glu Met Thr Lys Lys Gln Val
140               400               405               410
142 act ctg acc tgc atg gtc aca gac ttc atg cct gaa gac att tac gtg    1298
143 Thr Leu Thr Cys Met Val Thr Asp Phe Met Pro Glu Asp Ile Tyr Val
144               415               420               425
146 gag tgg acc aac aac ggg aaa aca gag cta aac tac aag aac act gaa    1346
147 Glu Trp Thr Asn Asn Gly Lys Thr Glu Leu Asn Tyr Lys Asn Thr Glu
148               430               435               440
150 cca gtc ctg gac tct gat ggt tct tac ttc atg tac agc aag ctg aga    1394
151 Pro Val Leu Asp Ser Asp Gly Ser Tyr Phe Met Tyr Ser Lys Leu Arg
152    445               450               455
154 gtg gaa aag aag aac tgg gtg gaa aga aat agc tac tcc tgt tca gtg    1442
155 Val Glu Lys Lys Asn Trp Val Glu Arg Asn Ser Tyr Ser Cys Ser Val
156 460               465               470               475
158 gtc cac gag ggt ctg cac aat cac cac acg act aag agc ttc tcc cgg    1490
159 Val His Glu Gly Leu His Asn His His Thr Thr Lys Ser Phe Ser Arg
160               480               485               490
162 act ccg ggt aaa tgatgactcg acctg                                   1517
163 Thr Pro Gly Lys
164               495
167 <210> SEQ ID NO: 2
168 <211> LENGTH: 495
169 <212> TYPE: PRT
170 <213> ORGANISM: Artificial Sequence
172 <220> FEATURE:
172 <223> OTHER INFORMATION: see item 6 on Error Summary Sheet
172 <400> 2                                        (same
173 Met Pro Cys Ser Arg Ala Leu Ile Leu Gly Val Leu Ala Leu Asn Thr   error in
174  1               5               10               15
176 Met Leu Ser Leu Cys Gly Gly Glu Asp Asp Ile Glu Ala Asp His Val  seqs. 4,6,8
177               20               25               30
179 Gly Phe Tyr Gly Thr Thr Val Tyr Gln Ser Pro Gly Asp Ile Gly Gln
180               35               40               45
182 Tyr Thr His Glu Phe Asp Gly Asp Glu Leu Phe Tyr Val Asp Leu Asp
183    50               55               60
185 Lys Lys Lys Thr Val Trp Arg Leu Pro Glu Phe Gly Gln Leu Ile Leu
186 65               70               75               80
188 Phe Glu Pro Gln Gly Gly Leu Gln Asn Ile Ala Ala Glu Lys His Asn
189               85               90               95
191 Leu Gly Ile Leu Thr Lys Arg Ser Asn Phe Thr Pro Ala Thr Asn Glu
192               100               105               110
```

W--> 172 (written annotations in right margin)

```
194 Ala Pro Gln Ala Thr Val Phe Pro Lys Ser Pro Val Leu Leu Gly Gln
195         115             120             125
197 Pro Asn Thr Leu Ile Cys Phe Val Asp Asn Ile Phe Pro Pro Val Ile
198         130             135             140
200 Asn Ile Thr Trp Leu Arg Asn Ser Lys Ser Val Thr Asp Gly Val Tyr
201 145             150             155             160
203 Glu Thr Ser Phe Leu Val Asn Arg Asp His Ser Phe His Lys Leu Ser
204         165             170             175
206 Tyr Leu Thr Phe Ile Pro Ser Asp Asp Asp Ile Tyr Asp Cys Lys Val
207         180             185             190
209 Glu His Trp Gly Leu Glu Glu Pro Val Leu Lys His Trp Glu Pro Glu
210         195             200             205
212 Ile Pro Ala Pro Met Ser Glu Leu Thr Glu Thr Gly Gly Gly Gly Ser
213         210             215             220
215 Thr Thr Ala Pro Ser Ala Gln Leu Glu Lys Glu Leu Gln Ala Leu Glu
216 225             230             235             240
218 Lys Glu Asn Ala Gln Leu Glu Trp Glu Leu Gln Ala Leu Glu Lys Glu
219         245             250             255
221 Leu Ala Gln Ala Ala Ser Glu Pro Arg Gly Pro Thr Ile Lys Pro Cys
222         260             265             270
224 Pro Pro Cys Lys Cys Pro Ala Pro Asn Leu Leu Gly Gly Pro Ser Val
225         275             280             285
227 Phe Ile Phe Pro Pro Lys Ile Lys Asp Val Leu Met Ile Ser Leu Ser
228         290             295             300
230 Pro Ile Val Thr Cys Val Val Val Asp Val Ser Glu Asp Asp Pro Asp
231 305             310             315             320
233 Val Gln Ile Ser Trp Phe Val Asn Asn Val Glu Val His Thr Ala Gln
234         325             330             335
236 Thr Gln Thr His Arg Glu Asp Tyr Asn Ser Thr Leu Arg Val Val Ser
237         340             345             350
239 Ala Leu Pro Ile Gln His Gln Asp Trp Met Ser Gly Lys Glu Phe Lys
240         355             360             365
242 Cys Lys Val Asn Asn Lys Asp Leu Pro Ala Pro Ile Glu Arg Thr Ile
243         370             375             380
245 Ser Lys Pro Lys Gly Ser Val Arg Ala Pro Gln Val Tyr Val Leu Pro
246 385             390             395             400
248 Pro Pro Glu Glu Glu Met Thr Lys Lys Gln Val Thr Leu Thr Cys Met
249         405             410             415
251 Val Thr Asp Phe Met Pro Glu Asp Ile Tyr Val Glu Trp Thr Asn Asn
252         420             425             430
254 Gly Lys Thr Glu Leu Asn Tyr Lys Asn Thr Glu Pro Val Leu Asp Ser
255         435             440             445
257 Asp Gly Ser Tyr Phe Met Tyr Ser Lys Leu Arg Val Glu Lys Lys Asn
258         450             455             460
260 Trp Val Glu Arg Asn Ser Tyr Ser Cys Ser Val Val His Glu Gly Leu
261 465             470             475             480
263 His Asn His His Thr Thr Lys Ser Phe Ser Arg Thr Pro Gly Lys
264         485             490             495
267 <210> SEQ ID NO: 3
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268 <211> LENGTH: 1485
269 <212> TYPE: DNA
270 <213> ORGANISM: Artificial Sequence
272 <220> FEATURE:
273 <223> OTHER INFORMATION: Description of Artificial Sequence:coding region
274       of SEQ ID NO:1
276 <220> FEATURE:
277 <221> NAME/KEY: CDS
278 <222> LOCATION: (1)..(1485)
280 <400> SEQUENCE: 3
281 atg ccg tgc agc aga gct ctg att ctg ggg gtc ctc gcc ctg aac acc   48
282 Met Pro Cys Ser Arg Ala Leu Ile Leu Gly Val Leu Ala Leu Asn Thr
283  1               5                  10                  15
285 atg ctc agc ctc tgc gga ggt gaa gac gac att gag gcc gac cac gta   96
286 Met Leu Ser Leu Cys Gly Gly Glu Asp Asp Ile Glu Ala Asp His Val
287              20                  25                  30
289 ggc ttc tat ggt aca act gtt tat cag tct cct gga gac att ggc cag  144
290 Gly Phe Tyr Gly Thr Thr Val Tyr Gln Ser Pro Gly Asp Ile Gly Gln
291          35                  40                  45
293 tac aca cat gaa ttt gat ggt gat gag ttg ttc tat gtg gac ttg gat  192
294 Tyr Thr His Glu Phe Asp Gly Asp Glu Leu Phe Tyr Val Asp Leu Asp
295      50                  55                  60
297 aag aag aaa act gtc tgg agg ctt cct gag ttt ggc caa ttg ata ctc  240
298 Lys Lys Lys Thr Val Trp Arg Leu Pro Glu Phe Gly Gln Leu Ile Leu
299  65                  70                  75                  80
301 ttt gag ccc caa ggt gga ctg caa aac ata gct gca gaa aaa cac aac  288
302 Phe Glu Pro Gln Gly Gly Leu Gln Asn Ile Ala Ala Glu Lys His Asn
303                  85                  90                  95
305 ttg gga atc ttg act aag agg tca aat ttc acc cca gct acc aat gag  336
306 Leu Gly Ile Leu Thr Lys Arg Ser Asn Phe Thr Pro Ala Thr Asn Glu
307              100                 105                 110
309 gct cct caa gcg act gtg ttc ccc aag tcc cct gtg ctg ctg ggt cag  384
310 Ala Pro Gln Ala Thr Val Phe Pro Lys Ser Pro Val Leu Leu Gly Gln
311          115                 120                 125
313 ccc aac acc ctt atc tgc ttt gtg gac aac atc ttc cca cct gtg atc  432
314 Pro Asn Thr Leu Ile Cys Phe Val Asp Asn Ile Phe Pro Pro Val Ile
315      130                 135                 140
317 aac atc aca tgg ctc aga aat agc aag tca gtc aca gac ggc gtt tat  480
318 Asn Ile Thr Trp Leu Arg Asn Ser Lys Ser Val Thr Asp Gly Val Tyr
319 145                 150                 155                 160
321 gag acc agc ttc ctc gtc aac cgt gac cat tcc ttc cac aag ctg tct  528
322 Glu Thr Ser Phe Leu Val Asn Arg Asp His Ser Phe His Lys Leu Ser
323              165                 170                 175
325 tat ctc acc ttc atc cct tct gat gat gac att tat gac tgc aag gtg  576
326 Tyr Leu Thr Phe Ile Pro Ser Asp Asp Asp Ile Tyr Asp Cys Lys Val
327          180                 185                 190
329 gag cac tgg ggc ctg gag gag ccg gtt ctg aaa cac tgg gaa cct gag  624
330 Glu His Trp Gly Leu Glu Glu Pro Val Leu Lys His Trp Glu Pro Glu
331          195                 200                 205
```

Input Set : **A:\seq list.txt**
Output Set: **N:\CRF4\12292005\J048116A.raw**

L:172 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:2, <213>
ORGANISM:Artificial Sequence
L:172 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:2, <213>
ORGANISM:Artificial Sequence
L:172 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:2,Line#:172
L:411 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:4, <213>
ORGANISM:Artificial Sequence
L:411 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:4, <213>
ORGANISM:Artificial Sequence
L:411 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:4,Line#:411
L:606 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:6, <213>
ORGANISM:Artificial Sequence
L:606 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:6, <213>
ORGANISM:Artificial Sequence
L:606 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:6,Line#:606
L:768 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:8, <213>
ORGANISM:Artificial Sequence
L:768 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:8, <213>
ORGANISM:Artificial Sequence
L:768 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:8,Line#:768